



SEQUENCE LISTING

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<120> Irelp, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME

<130> UMV-1584

<140> US 09/357,273

<141> 1999-07-20

<150> US 60/093,526

<151> 1998-07-21

<160> 13

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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Met Pro Ala Arg Arg Leu
1 5

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Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly Leu Gly Ile Phe Gly Ser
10 15 20

acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210
Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu
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gat gga agt ttg cat gct gtc agc aag agg aca ggc tca atc aaa tgg 258
Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp
40 45 50

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Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu
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Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly
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agc aag aat aat gaa ggc ctg acg aaa ctt cct ttt acc atc cca gaa 402
Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu Pro Phe Thr Ile Pro Glu
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Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile Asp Leu Leu Thr Gly Glu	
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Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala Asp Ser Leu Cys Pro Ser	
135 140 145 150	
acc tct ctt ctg tat ctt ggg cga aca gaa tac acc atc acc atg tac	594
Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu Tyr Thr Ile Thr Met Tyr	
155 160 165	
gac acc aaa acc cga gag ctc cgg tgg aat gcc acc tac ttt gac tat	642
Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn Ala Thr Tyr Phe Asp Tyr	
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gcg gcc tca ctg cct gag gac gaa ggg gac tac aag atg tcc cac ttt	690
Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp Tyr Lys Met Ser His Phe	
185 190 195	
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Val Ser Asn Gly Asp Gly Leu Val Val Thr Val Asp Ser Glu Ser Gly	
200 205 210	
gac gtc ctg tgg atc caa aac tac gcc tcc cct gtg gtg gcc ttt tat	786
Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser Pro Val Val Ala Phe Tyr	
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gtc tgg cag cgg gag ggt ctg agg aag gtg atg cac atc aat gtc gct	834
Val Trp Gln Arg Glu Gly Leu Arg Lys Val Met His Ile Asn Val Ala	
235 240 245	
gtg gag acc ctg cgc tat ctg acc ttc atg tct ggg gag gtg ggg cgc	882
Val Glu Thr Leu Arg Tyr Leu Thr Phe Met Ser Gly Glu Val Gly Arg	
250 255 260	
atc aca aag tgg aag tac ccg ttc ccc aag gag aca gag gcc aag agc	930
Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys Glu Thr Glu Ala Lys Ser	
265 270 275	
aag ctg acg ccc act ctg tat gtt ggg aaa tac tct acc agc ctc tat	978
Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys Tyr Ser Thr Ser Leu Tyr	
280 285 290	
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Ala Ser Pro Ser Met Val His Glu Gly Val Ala Val Val Pro Arg Gly	
295 300 305 310	
agc aca ctt cct ttg ctg gaa ggg ccc cag act gat ggc gtc acc atc	1074
Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln Thr Asp Gly Val Thr Ile	
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Gly Asp Lys Gly Glu Cys Val Ile Thr Pro Ser Thr Asp Val Lys Phe	
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Trp Leu Leu Ile Gly His His Glu Thr Pro Leu Ser Ala Ser Thr Lys			
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Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe Glu Glu Val Ile Asn Leu			
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Val Asp Gln Thr Ser Glu Asn Ala Pro Thr Thr Val Ser Arg Asp Val			
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Glu Glu Lys Pro Ala His Ala Pro Ala Arg Pro Glu Ala Pro Val Asp			
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Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr Pro Leu Ser Met His Gln			
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Gln Gln Gln Leu Gln His Gln Gln Phe Gln Lys Glu Leu Glu Lys Ile			
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Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu Pro Phe His Pro Pro Gly			
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His Ser Leu Cys Ser Gly Ser Ser Ala Ser Lys Ala Gly Ser Ser Pro			
	535	540	545
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Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu Thr Ser Val Val Ile Val			
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Gly Lys Ile Ser Phe Cys Pro Lys Asp Val Leu Gly His Gly Ala Glu			
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Gly Thr Ile Val Tyr Arg Gly Met Phe Asp Asn Arg Asp Val Ala Val			
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acg gag aag gac cgg caa ttc cag tac att gcc atc gag ctg tgt gca Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile Ala Ile Glu Leu Cys Ala 635 640 645	2034
gcc acc ctg caa gag tat gtg gag cag aag gac ttt gcg cat ctc ggc Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly 650 655 660	2082
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ctc cac tcc ctc aac atc gtt cac aga gac cta aag cca cac aac atc Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile 680 685 690	2178
ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser 695 700 705 710	2226
gac ttt ggc ctc tgc aag aag ctg gca gtg ggc aga cac agt ttc agc Asp Phe Gly Leu Cys Lys Lys Leu Ala Val Gly Arg His Ser Phe Ser 715 720 725	2274
cgc cga tct ggg gtg cct ggc aca gaa ggc tgg atc gct cca gag atg Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met 730 735 740	2322
ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe 745 750 755	2370
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gaa ttg ata gag aag atg att gcg atg gat cct cag aaa cgc ccc tca Glu Leu Ile Glu Lys Met Ile Ala Met Asp Pro Gln Lys Arg Pro Ser 810 815 820	2562
gcg aac gac gtg ctc aaa cac ccg ttc ttc tgg agc cta gag aag cag Ala Asn Asp Val Leu Lys His Pro Phe Phe Trp Ser Leu Glu Lys Gln 825 830 835	2610

ctc cag ttc ttc cag gac gtg agc gac aga ata gaa aag gaa tcc ctg 2658
 Leu Gln Phe Phe Gln Asp Val Ser Asp Arg Ile Glu Lys Glu Ser Leu
 840 845 850

gat ggc ccg atc gtg aag cag tta gag aga ggc ggg aga gcc gtg gtg 2706
 Asp Gly Pro Ile Val Lys Gln Leu Glu Arg Gly Gly Arg Ala Val Val
 855 860 865 870

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 Lys Met Asp Trp Arg Glu Asn Ile Thr Asp Pro Leu Gln Thr Asp Leu
 875 880 885

cgt aaa ttc agg acc tat aaa ggt ggt tct gtc aga gat ctc ctc cga 2802
 Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser Val Arg Asp Leu Leu Arg
 890 895 900

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 Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Ala Glu Val
 905 910 915

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 Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp Phe Val Cys Tyr Phe Thr
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 Ser Arg Phe Pro His Leu Leu Ala His Thr Tyr Arg Ala Met Glu Leu
 935 940 945 950

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 Cys Ser His Glu Arg Leu Phe Gln Pro Tyr Tyr Phe His Glu Pro Pro
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 970 975

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<213> Homo sapiens

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 35 40 45
 Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val
 50 55 60
 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
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 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
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 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
 115 120 125
 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala
 130 135 140
 Asp Ser Leu Cys Pro Ser Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu
 145 150 155 160
 Tyr Thr Ile Thr Met Tyr Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn
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 Ala Thr Tyr Phe Asp Tyr Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp
 180 185 190
 Tyr Lys Met Ser His Phe Val Ser Asn Gly Asp Gly Leu Val Val Thr
 195 200 205
 Val Asp Ser Glu Ser Gly Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser
 210 215 220
 Pro Val Val Ala Phe Tyr Val Trp Gln Arg Glu Gly Leu Arg Lys Val
 225 230 235 240
 Met His Ile Asn Val Ala Val Glu Thr Leu Arg Tyr Leu Thr Phe Met
 245 250 255
 Ser Gly Glu Val Gly Arg Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys
 260 265 270
 Glu Thr Glu Ala Lys Ser Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys
 275 280 285
 Tyr Ser Thr Ser Leu Tyr Ala Ser Pro Ser Met Val His Glu Gly Val
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 Ala Val Val Pro Arg Gly Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln

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Ser Thr Asp Val	Lys Phe Asp Pro Gly	Leu Lys Ser Lys	Asn Lys Leu			
	340		345			350
Asn Tyr Leu Arg	Asn Tyr Trp Leu Leu	Ile Gly His His	Glu Thr Pro			
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Leu Ser Ala Ser	Thr Lys Met Leu Glu	Arg Phe Pro Asn	Asn Leu Pro			
	370		375			380
Lys His Arg Glu	Asn Val Ile Pro Ala	Asp Ser Glu Lys	Lys Ser Phe			
	385		390			395
Glu Glu Val Ile	Asn Leu Val Asp Gln	Thr Ser Glu Asn	Ala Pro Thr			
	405		410			415
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Pro Glu Ala Pro	Val Asp Ser Met Leu	Lys Asp Met Ala	Thr Ile Ile			
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Leu Ser Thr Phe	Leu Leu Ile Gly Trp	Val Ala Phe Ile	Ile Thr Tyr			
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Pro Leu Ser Met	His Gln Gln Gln	Leu Gln His Gln	Gln Phe Gln			
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Lys Glu Leu Glu	Lys Ile Gln Leu	Leu Gln Gln Gln	Gln Gln Leu			
	485		490			495
Pro Phe His Pro	Pro Gly Asp Thr	Ala Gln Asp Gly	Glu Leu Leu	Asp		
	500		505			510
Thr Ser Gly Pro	Tyr Ser Glu Ser	Ser Gly Thr Ser	Ser Pro Ser	Thr		
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Ser Pro Arg Ala	Ser Asn His Ser	Leu Cys Ser Gly	Ser Ser Ala	Ser		
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Lys Ala Gly Ser	Ser Pro Ser Leu	Glu Gln Asp Asp	Gly Asp Glu	Glu		
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Thr Ser Val Val	Ile Val Gly Lys	Ile Ser Phe Cys	Pro Lys Asp	Val		
	565		570			575
Leu Gly His Gly	Ala Glu Gly Thr	Ile Val Tyr Arg	Gly Met Phe	Asp		
	580		585			590
Asn Arg Asp Val	Ala Val Lys Arg	Ile Leu Pro Glu	Cys Phe Ser	Phe		
	595		600			605
Ala Asp Arg Glu	Val Gln Leu Leu	Arg Glu Ser Asp	Glu His Pro	Asn		
	610		615			620
Val Ile Arg Tyr	Phe Cys Thr Glu	Lys Asp Arg Gln	Phe Gln Tyr	Ile		
	625		630			635
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 645 650 655
 Asp Phe Ala His Leu Gly Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr
 660 665 670
 Thr Ser Gly Leu Ala His Leu His Ser Leu Asn Ile Val His Arg Asp
 675 680 685
 Leu Lys Pro His Asn Ile Leu Ile Ser Met Pro Asn Ala His Gly Lys
 690 695 700
 Ile Lys Ala Met Ile Ser Asp Phe Gly Leu Cys Lys Lys Leu Ala Val
 705 710 715 720
 Gly Arg His Ser Phe Ser Arg Arg Ser Gly Val Pro Gly Thr Glu Gly
 725 730 735
 Trp Ile Ala Pro Glu Met Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr
 740 745 750
 Tyr Thr Val Asp Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Val
 755 760 765
 Ser Glu Gly Ser His Pro Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn
 770 775 780
 Ile Leu Leu Gly Ala Cys Ser Leu Asp Cys Leu His Pro Glu Lys His
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 Glu Asp Val Ile Ala Arg Glu Leu Ile Glu Lys Met Ile Ala Met Asp
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 Pro Gln Lys Arg Pro Ser Ala Asn Asp Val Leu Lys His Pro Phe Phe
 820 825 830
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 Ile Glu Lys Glu Ser Leu Asp Gly Pro Ile Val Lys Gln Leu Glu Arg
 850 855 860
 Gly Gly Arg Ala Val Val Lys Met Asp Trp Arg Glu Asn Ile Thr Asp
 865 870 875 880
 Pro Leu Gln Thr Asp Leu Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser
 885 890 895
 Val Arg Asp Leu Leu Arg Ala Met Arg Asn Lys Lys His His Tyr Arg
 900 905 910
 Glu Leu Pro Ala Glu Val Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp
 915 920 925
 Phe Val Cys Tyr Phe Thr Ser Arg Phe Pro His Leu Leu Ala His Thr
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Leu

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Ser	Ile	Gly	Asp	Asp	Glu	Glu	Lys	Thr	Ser	Ser	Thr	Ile	Leu	Val	Ser
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Thr	Ile	Asp	Gly	Arg	Leu	Arg	Ala	Leu	Asp	Ser	Glu	Thr	Gly	Glu	Ile
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Val	Leu	Lys	Asn	Ser	Ser	Leu	Lys	Lys	Leu	Pro	Phe	Asn	Ile	Pro	Gln
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Leu	Val	His	Ala	Ser	Pro	Cys	Lys	Gly	Asn	Asp	Gly	Ile	Leu	Tyr	Ala
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Gly	Ser	Lys	Lys	Asp	Val	Trp	Phe	Gly	Ile	Asp	Pro	Lys	Thr	Gly	Leu
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Lys	Val	Glu	Tyr	Ile	Leu	Leu	Asn	Ile	Ser	Asp	Lys	Ile	Leu	Phe	Leu
145					150					155					160
Gln	Val	Glu	Thr	Leu	Ser	Ser	Ala	Ser	Ala	Asp	Arg	Ile	Cys	Pro	Ala
				165					170					175	
Asn	Gln	Lys	Gln	Thr	Ile	Phe	Leu	Gly	Arg	Thr	Glu	Tyr	Arg	Val	Ser
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Met	Phe	Asp	Glu	Lys	Asn	Arg	Gly	Lys	Thr	Trp	Asn	Ala	Thr	Phe	Asn
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Asp	Tyr	Ser	Ala	His	Leu	Leu	Pro	Glu	Val	Asn	Thr	Trp	Pro	Phe	Lys
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His	Tyr	Ala	Ser	Ser	Ser	His	Gly	Tyr	Ile	Leu	Thr	Phe	Asp	Arg	Glu
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Thr	Gly	Glu	Met	Arg	Trp	Glu	Gln	Asp	Leu	Lys	Gln	Pro	Val	Val	Ala
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 260 265 270
 Met Gly Lys Glu Thr Met Glu Asn Val Ala Lys Asn Ile Phe Thr Val
 275 280 285
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 Thr Ser Leu Thr Asn Gln Phe Phe Pro Ala Leu Phe Val Gly Glu Ser
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 Ser Phe Gly Leu Tyr Ala Ile Glu Ala Leu Val Asp His Gln Thr Ile
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 Thr Tyr Ser Pro Lys Leu Leu Gly Pro Pro Leu Leu Glu Gly Pro Ala
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 Pro Ile Ala Leu Thr Glu Met Glu Lys Glu Glu Tyr Leu Pro Pro Arg
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 Arg Pro Ile Ile Arg Asn Ile Pro Pro Ser Ile Thr His Lys Thr Ser
 370 375 380
 Asp Gly Glu Tyr Leu Leu Leu Gly Tyr His Asp Arg Pro Met Met Thr
 385 390 395 400
 Met Ala Thr Ile Ile Pro Thr Arg Tyr Pro Val Pro Gly Pro His Lys
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 Ala Ile Gly Ser Thr Ile Glu Arg Pro Pro Pro Gln Leu Leu Gly Pro
 420 425 430
 Val Glu Pro Gln Lys His Glu Asp Thr Ser Phe Ile Leu Leu Leu Leu
 435 440 445
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 450 455 460
 Leu Leu Leu Thr Val Ile Trp Gln Cys Gly Arg Gln Trp Asp Gln Gln
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 Lys Ser Thr Ser Arg Met Asp Ser Phe Glu Ile Val Asn Asn Pro Gly
 485 490 495
 Glu Ser Arg Ser Ala Gln Thr Ser Lys Gln Ser Asn Arg Gly Ser Phe
 500 505 510
 Gly Trp Ala Asn Arg Lys Ile Glu Ile Pro Glu Gly Trp Met Ala Val
 515 520 525
 Gly Ser Lys Leu Met Tyr Ser Pro Ser Asp Ile Leu Gly Thr Gly Cys
 530 535 540
 Glu Gly Thr Val Val Tyr Arg Gly Thr Phe Asp Gly Arg Glu Val Ala
 545 550 555 560
 Val Lys Arg Val Val Ser Glu Phe Val Lys Phe Ala His Arg Glu Ala
 565 570 575
 Asp Leu Leu Arg Glu Ser Asp Thr His Pro His Val Ile Arg Tyr Phe

580										585					590				
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		595					600					605							
Ile	Ala	Ser	Leu	Asn	Asp	Tyr	Val	Glu	Gln	Lys	Glu	Val	Gln	Gln	Asn				
	610					615					620								
Val	Thr	Ile	Ala	Leu	Arg	Asp	Ile	Met	Lys	Gln	Ala	Thr	Asp	Gly	Leu				
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Ala	His	Leu	His	Ala	Ser	Lys	Ile	Val	His	Arg	Asp	Met	Lys	Pro	Gln				
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Asn	Val	Leu	Ile	Thr	Met	Ala	Ser	Gln	Arg	Gly	Glu	Met	Arg	Ala	Val				
			660					665					670						
Ile	Ser	Asp	Phe	Gly	Leu	Cys	Lys	Arg	Val	Gln	Pro	Gly	Lys	Asn	Ser				
		675					680					685							
Ile	Ser	Arg	Gly	Ile	Ala	Ser	Gly	Leu	Ala	Gly	Thr	Asp	Gly	Trp	Ile				
		690				695					700								
Ala	Pro	Glu	Val	Leu	Ile	Ser	Ala	Ser	Thr	Ser	Tyr	Pro	Val	Asp	Ile				
705					710					715					720				
Phe	Ser	Leu	Gly	Cys	Ile	Phe	Tyr	Tyr	Val	Leu	Thr	Ser	Gly	Thr	His				
				725					730					735					
Pro	Phe	Gly	Lys	Ser	Leu	His	Arg	Gln	Ala	Asn	Ile	Val	Asn	Gly	Glu				
			740					745					750						
Tyr	Thr	Leu	Asn	Lys	Leu	Ala	Asp	Leu	Asp	Asp	Trp	Ser	Leu	Ala	Asp				
		755					760					765							
Asp	Leu	Ile	Ser	Ser	Met	Leu	Asn	Val	Glu	Pro	Leu	His	Arg	Leu	Thr				
	770					775					780								
Ala	Asp	Ala	Val	Leu	Asn	His	Pro	Phe	Phe	Trp	Thr	Ser	Glu	Lys	Arg				
785					790					795					800				
Leu	Ala	Tyr	Phe	Ser	Asp	Val	Ser	Asp	Arg	Val	Glu	Lys	Glu	Glu	Asp				
				805					810					815					
Asn	Ser	Pro	Val	Val	Arg	Arg	Ile	Glu	Thr	Asp	Ala	Arg	Ile	Val	Val				
			820					825					830						
Cys	Gly	Gly	Trp	Arg	Glu	Lys	Ile	Cys	Asp	Ala	Leu	Lys	Glu	Asp	Leu				
		835					840					845							
Arg	Lys	Phe	Arg	Thr	Tyr	Lys	Ser	Phe	Ser	Val	Arg	Asp	Leu	Leu	Arg				
	850					855					860								
Ala	Met	Arg	Asn	Lys	Lys	His	His	Tyr	Arg	Glu	Leu	Pro	Glu	Asp	Val				
865					870					875					880				
Arg	Gln	Ser	Leu	Gly	Asp	Ile	Pro	Asp	Gln	Phe	Leu	His	Tyr	Phe	Thr				
				885					890					895					
Ser	Arg	Phe	Pro	Arg	Leu	Leu	Leu	His	Val	Tyr	Lys	Ala	Thr	Glu	Tyr				
			900					905					910						

Cys Ser Gly Glu Ala Val Phe Lys Arg Tyr Tyr Ser Asp Asp Val Arg
915 920 925

Ala Arg Met Tyr Pro Ile Val Glu Glu Glu Glu Arg Val Arg Lys Lys
930 935 940

Ile Lys Glu Glu Met Ala Asn Glu Val Trp Ala Arg Ala Pro Lys Pro
945 950 955 960

Val Glu Gln Arg Thr Pro Leu Lys Leu Asp Lys Arg Asn Ile Lys Lys
965 970 975

Lys Ser Asn Pro Asn Thr Asp
980

<210> 4

<211> 443

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

Leu Val Val Ser Cys Lys Ile Leu Gly Tyr Gly Ser Ser Gly Thr Val
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Val Phe Gln Gly Ser Phe Gln Gly Arg Pro Val Ala Val Lys Arg Met
20 25 30

Leu Ile Asp Phe Cys Asp Ile Ala Leu Met Glu Ile Lys Leu Leu Thr
35 40 45

Glu Ser Asp Asp His Pro Asn Val Ile Arg Tyr Tyr Cys Ser Glu Thr
50 55 60

Thr Asp Arg Phe Leu Tyr Ile Ala Leu Glu Leu Cys Asn Leu Asn Leu
65 70 75 80

Gln Asp Leu Val Glu Ser Lys Asn Val Ser Asp Glu Asn Leu Lys Leu
85 90 95

Gln Lys Glu Tyr Asn Pro Ile Ser Leu Leu Arg Gln Ile Ala Ser Gly
100 105 110

Val Ala His Leu His Ser Leu Lys Ile Ile His Arg Asp Leu Lys Pro
115 120 125

Gln Asn Ile Leu Val Ser Thr Ser Ser Arg Phe Thr Ala Asp Gln Gln
130 135 140

Thr Gly Ala Glu Asn Leu Arg Ile Leu Ile Ser Asp Phe Gly Leu Cys
145 150 155 160

Lys Lys Leu Asp Ser Gly Gln Ser Ser Phe Arg Thr Asn Leu Asn Asn
165 170 175

Pro Ser Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu Glu Glu Ser
180 185 190

Asn Asn Leu Gln Cys Gln Val Glu Thr Glu His Ser Ser Ser Arg His
195 200 205

Thr Val Val Ser Ser Asp Ser Phe Tyr Asp Pro Phe Thr Lys Arg Arg
 210 215 220

Leu Thr Arg Ser Ile Asp Ile Phe Ser Met Gly Cys Val Phe Tyr Tyr
 225 230 235 240

Ile Leu Ser Lys Gly Lys His Pro Phe Gly Asp Lys Tyr Ser Arg Glu
 245 250 255

Ser Asn Ile Ile Arg Gly Ile Phe Ser Leu Asp Glu Met Lys Cys Leu
 260 265 270

His Asp Arg Ser Leu Ile Ala Glu Ala Thr Asp Leu Ile Ser Gln Met
 275 280 285

Ile Asp His Asp Pro Leu Lys Arg Pro Thr Ala Met Lys Val Leu Arg
 290 295 300

His Pro Leu Phe Trp Pro Lys Ser Lys Lys Leu Glu Phe Leu Leu Lys
 305 310 315 320

Val Ser Asp Arg Leu Glu Ile Glu Asn Arg Asp Pro Pro Ser Ala Leu
 325 330 335

Leu Met Lys Phe Asp Ala Gly Ser Asp Phe Val Ile Pro Ser Gly Asp
 340 345 350

Trp Thr Val Lys Phe Asp Lys Thr Phe Met Asp Asn Leu Glu Arg Tyr
 355 360 365

Arg Lys Tyr His Ser Ser Lys Leu Met Asp Leu Leu Arg Ala Leu Arg
 370 375 380

Asn Lys Tyr His His Phe Met Asp Leu Pro Glu Asp Ile Ala Glu Leu
 385 390 395 400

Met Gly Pro Val Pro Asp Gly Phe Tyr Asp Tyr Phe Thr Lys Arg Phe
 405 410 415

Pro Asn Leu Leu Ile Gly Val Tyr Met Ile Val Lys Glu Asn Leu Ser
 420 425 430

Asp Asp Gln Ile Leu Arg Glu Phe Leu Tyr Ser
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<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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Ile Ser Asp Phe Gly Leu Cys Lys
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<210> 6

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<220>
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cgccatgcc

9

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<221> misc_feature
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<222> 4,9,13,16
<223> N may be Adenine or Guanine

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<222> 7,10,19,22
<223> N may be any nucleotide

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24

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1 5

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<212> DNA

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21

<210> 11

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<223> Description of Artificial Sequence: Primer

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<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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cggaattcat cacctatccc ctgagcatg

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<210> 13

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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cggaattctc agagggcgtc tggagtca

28